

A woman with short, light-colored hair, wearing a white lab coat and a small hoop earring, is shown in profile, focused on her work. She is holding a pipette. The background is a blurred laboratory setting with various pieces of equipment and windows. The overall image has a light blue/teal tint.

Reprogramming of 24 patient fibroblast samples: QC analysis 3/3 (Part 1)

05-01-2024

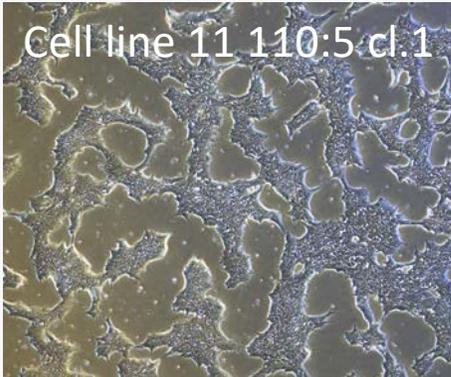
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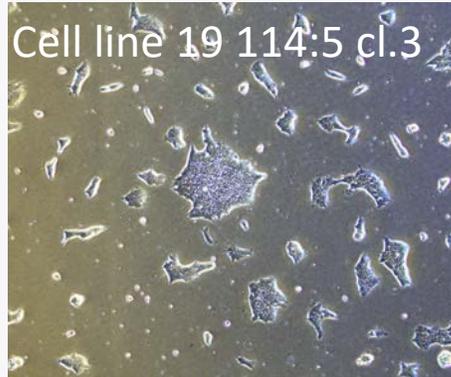
Morphology

Morphology of iPSCs 24 hours after thawing*:

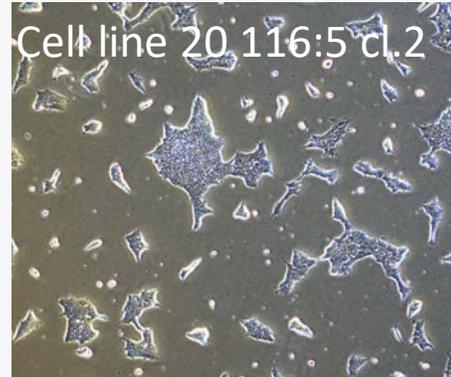
hPSCreg ID
SUHi013-A



hPSCreg ID
SUHi020-A



hPSCreg ID
SUHi021-A

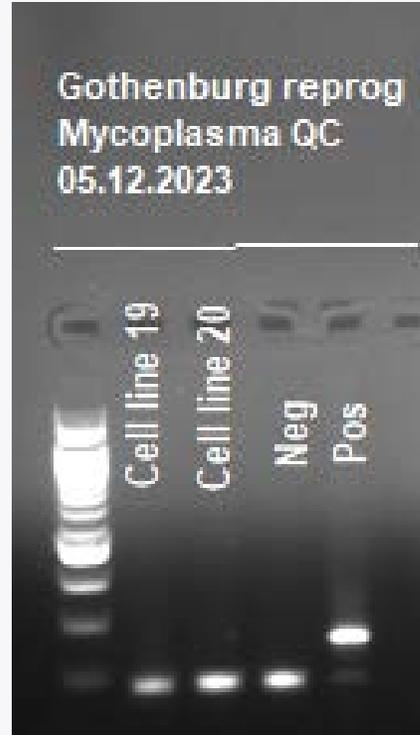
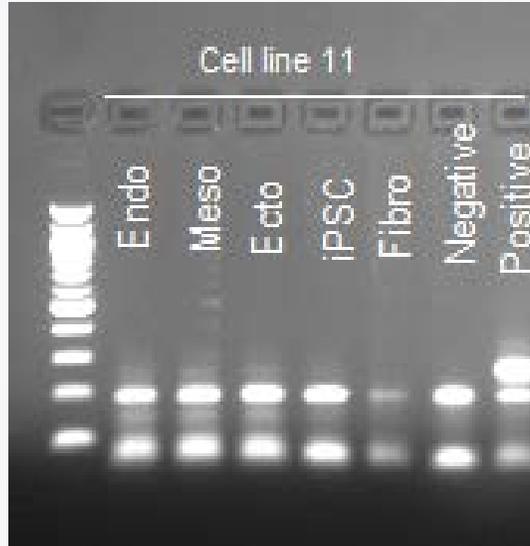


*Photos of the morphology of the iPSC lines before banking will be sent in a separate format (photos are too heavy to be included here).

QC Overview

| hPSCreg ID | Line ID | Clone | Mycoplasma | Sterility | Trilineage diff. |
|------------|--------------------|-------|------------|-----------|------------------|
| SUHi013-A | Cell line 11 110:5 | 1 | Passed | Passed | Passed |
| SUHi020-A | Cell line 19 114:5 | 3 | Passed | Passed | Passed |
| SUHi021-A | Cell line 20 116:5 | 2 | Passed | Passed | Passed |

Mycoplasma test



| hPSCreg ID | Line ID | Clone |
|------------|-----------------------|-------|
| SUHi013-A | Cell line 11 110:5 | 1 |
| SUHi020-A | Cell line 19 114:5 | 3 |
| SUHi021-A | Cell line 20 116:5 | 2 |

Sterility test

No contamination was detected in any of the lines 48 hours after thawing (data not shown).

Trilineage differentiation

| hPSCreg ID | SAMPLES | Fold over reference sample | | | |
|------------|------------------------------|------------------------------|------------------------------|---------------------|-------|
| | | GATA4 (Endo and Meso marker) | CXCR4 (Meso and Endo marker) | Pax 6 (Ecto marker) | GAPDH |
| SUHi013-A | Cell line 11 110:5 cl 1 iPSC | 1 | 1 | 1 | 1 |
| SUHi020-A | Cell line 19 114:5 cl 3 iPSC | 1 | 1 | 1 | 1 |
| SUHi021-A | Cell line 20 116:5 cl 2 iPSC | 1 | 1 | 1 | 1 |
| SUHi013-A | Cell line 11 110:5 cl 1 Endo | 1084,890209 | 46,3126156 | 7,981537412 | 1 |
| SUHi020-A | Cell line 19 114:5 cl 3 Endo | 4781,784284 | 87,02351186 | 3,758090997 | 1 |
| SUHi021-A | Cell line 20 116:5 cl 2 Endo | 1348,057825 | 89,47007579 | 42,91271673 | 1 |
| SUHi013-A | Cell line 11 110:5 cl 1 Meso | 283,3942481 | 217,7707932 | 0,065607293 | 1 |
| SUHi020-A | Cell line 19 114:5 cl 3 Meso | 1237,603386 | 449,8603275 | 0,069991975 | 1 |
| SUHi021-A | Cell line 20 116:5 cl 2 Meso | 901,8018546 | 473,318226 | 1,598442299 | 1 |
| SUHi013-A | Cell line 11 110:5 cl 1 Ecto | 0,117440344 | 39,48775199 | 4502,987216 | 1 |
| SUHi020-A | Cell line 19 114:5 cl 3 Ecto | 0,190782401 | 22,67975788 | 1584,706553 | 1 |
| SUHi021-A | Cell line 20 116:5 cl 2 Ecto | 0,108317131 | 19,38228379 | 10108,86451 | 1 |

Fold over reference sample is based on the formula:

$$2^{-\Delta\Delta Ct} = 2^{-(\Delta Ct \text{ target tissue} - \Delta Ct \text{ reference tissue})}$$

Where:

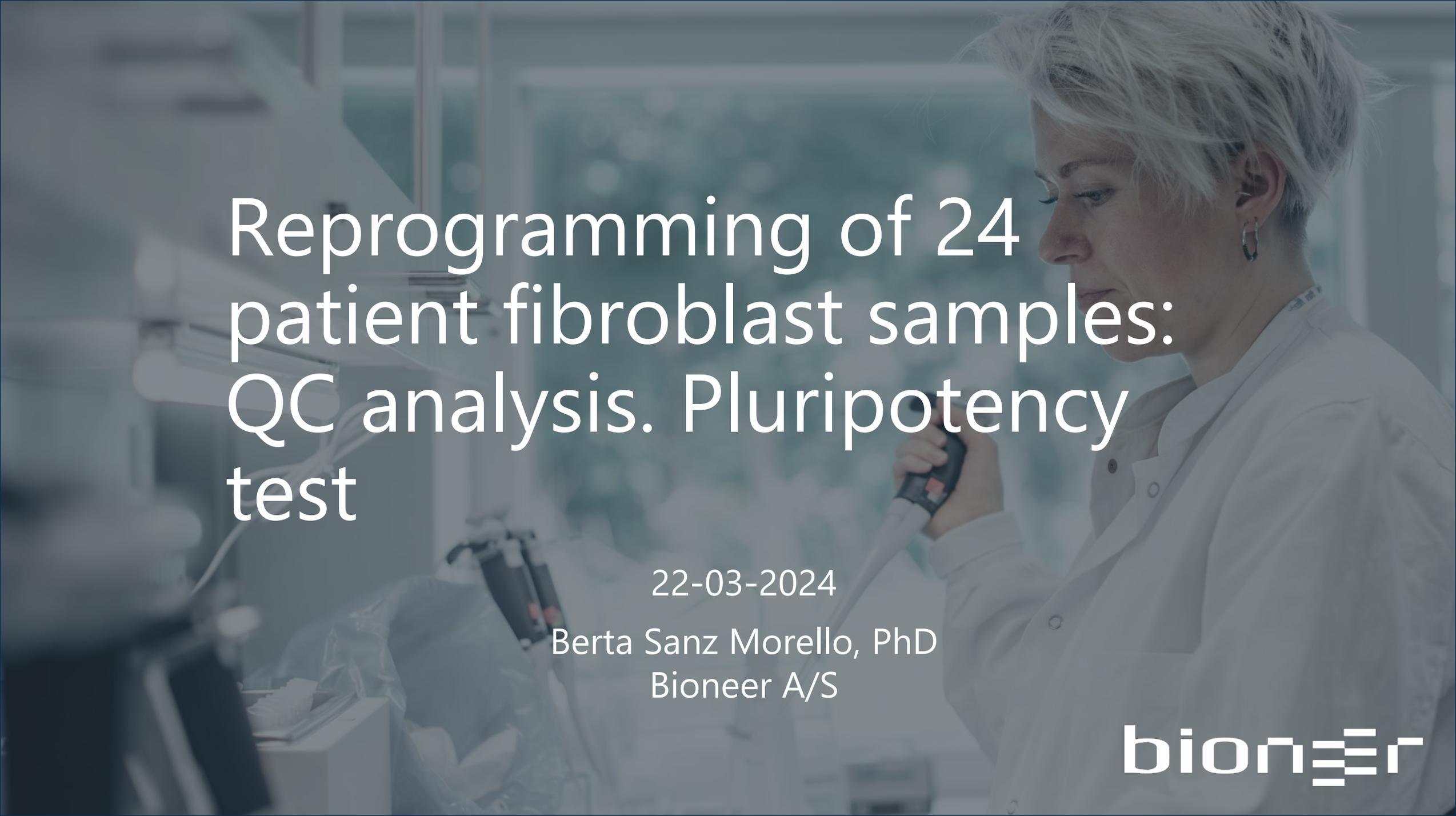
ΔCt = Ct gene of interest – Ct house keeping gene

Target tissue = endo, ecto or mesoderm
 Reference tissue = undifferentiated iPSCs
 Gene of interest = GATA4, CXCR4, or Pax6
 Housekeeping gene = GAPDH

Trilineage differentiation

| hPSCreg ID | SAMPLES | Fold over reference sample | | | |
|------------|------------------------------|------------------------------|------------------------------|---------------------|-------|
| | | GATA4 (Endo and Meso marker) | CXCR4 (Meso and Endo marker) | Pax 6 (Ecto marker) | GAPDH |
| SUHi013-A | Cell line 11 110:5 cl 1 iPSC | 1 | 1 | 1 | 1 |
| SUHi020-A | Cell line 19 114:5 cl 3 iPSC | 1 | 1 | 1 | 1 |
| SUHi021-A | Cell line 20 116:5 cl 2 iPSC | 1 | 1 | 1 | 1 |
| SUHi013-A | Cell line 11 110:5 cl 1 Endo | 1084,890209 | 46,3126156 | 7,981537412 | 1 |
| SUHi020-A | Cell line 19 114:5 cl 3 Endo | 4781,784284 | 87,02351186 | 3,758090997 | 1 |
| SUHi021-A | Cell line 20 116:5 cl 2 Endo | 1348,057825 | 89,47007579 | 42,91271673 | 1 |
| SUHi013-A | Cell line 11 110:5 cl 1 Meso | 283,3942481 | 217,7707932 | 0,065607293 | 1 |
| SUHi020-A | Cell line 19 114:5 cl 3 Meso | 1237,603386 | 449,8603275 | 0,069991975 | 1 |
| SUHi021-A | Cell line 20 116:5 cl 2 Meso | 901,8018546 | 473,318226 | 1,598442299 | 1 |
| SUHi013-A | Cell line 11 110:5 cl 1 Ecto | 0,117440344 | 39,48775199 | 4502,987216 | 1 |
| SUHi020-A | Cell line 19 114:5 cl 3 Ecto | 0,190782401 | 22,67975788 | 1584,706553 | 1 |
| SUHi021-A | Cell line 20 116:5 cl 2 Ecto | 0,108317131 | 19,38228379 | 10108,86451 | 1 |

All iPSC lines tested were able to differentiate to the 3 germ layers.

A woman with short blonde hair, wearing a white lab coat and a small hoop earring, is shown in profile from the chest up. She is holding a pipette and looking down at it. The background is a blurred laboratory setting with various pieces of equipment and glassware. The entire image has a light blue tint.

Reprogramming of 24 patient fibroblast samples: QC analysis. Pluripotency test

22-03-2024

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Pluripotency analysis

| hPSCreg ID | SAMPLES | OCT4 | NANOG | GAPDH |
|------------|-------------------------------|------|-------|-------|
| SUHi001-A | Cell line 1 143 cl 1 | 1.19 | 0.95 | 1 |
| SUHi002-A | Cell line 2 145 cl 2 | 0.99 | 0.92 | 1 |
| SUHi003-A | Cell line 3 146 cl 1 | 1.23 | 0.88 | 1 |
| SUHi004-A | Cell line 4 152 cl 3 | 1.00 | 0.56 | 1 |
| SUHi005-A | Cell line 5 165 cl 2 | 0.98 | 0.75 | 1 |
| SUHi006-A | Cell line 6 169 cl 3 | 1.16 | 0.65 | 1 |
| SUHi007-A | Cell line 7 102:5 cl 1 | 1.41 | 0.75 | 1 |
| SUHi008-A | Cell line 8 104:5 cl 2 | 1.21 | 0.94 | 1 |
| SUHi010-A | Cell line 9 117:5 cl 3 | 1.16 | 1.11 | 1 |
| SUHi014-A | Cell line 10 120:5 cl 3 | 0.92 | 0.62 | 1 |
| SUHi013-A | Cell line 11 110:5 cl 1 | 0.81 | 0.82 | 1 |
| SUHi009-A | Cell line 12 105:5 cl 3 | 1.20 | 0.77 | 1 |
| SUHi011-A | Cell line 13 151 cl 1 | 1.11 | 0.79 | 1 |
| SUHi012-A | Cell line 14 163 cl 2 | 1.01 | 0.87 | 1 |
| SUHi015-A | Cell line 15 141 cl 3 | 0.65 | 0.84 | 1 |
| SUHi016-A | Cell line 16 142:3 cl 1 | 0.80 | 1.15 | 1 |
| SUHi018-A | Cell line 17 RES168 cl 1 | 0.91 | 0.89 | 1 |
| SUHi020-A | Cell line 19 RES114:5 cl 3 | 1.13 | 0.66 | 1 |
| SUHi021-A | Cell line 20 RES116:5 cl 2 | 0.74 | 0.73 | 1 |
| SUHi022-A | Cell line 21 RES118:5 cl 1 | 0.80 | 0.60 | 1 |
| SUHi023-A | Cell line 22 RES121:5 cl 5 | 0.81 | 0.38 | 1 |
| SUHi024-A | Cell line 23 RES174 cl 4 | 0.78 | 0.47 | 1 |
| SUHi017-A | Cell line 24 RES158 cl 4 | 0.93 | 0.55 | 1 |
| Control | Control iPSC line: BIONi010-C | 1 | 1 | 1 |

Fold over reference sample is based on the formula:

$$2^{-\left(\Delta\text{Ct target tissue} - \Delta\text{Ct reference tissue}\right)}$$

Where:

$\Delta\text{Ct} = \text{Ct gene of interest} - \text{Ct house keeping gene}$

Target tissue = reprogrammed cell lines

Reference tissue = iPSC line BIONi010-C

Genes of interest = OCT4, NANOG

Housekeeping gene = GAPDH

All reprogrammed lines tested showed pluripotency ability.